## SEQUENCE LISTING

- <110> ROSENBLUM, MICHAEL G. CHEUNG, LAWRENCE
- <120> MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF MAKING THEEOF
- <130> CLFR:007US
- <140> UNKNOWN
- <141> 2002-02-12
- <150> 60/268,402
- <151> 2001-02-12
- <160> 11
- <170> PatentIn Ver. 2.1
- <210> 1
- <211> 316
- <212> PRT
- <213> Gelonium multiflorum
- <400> 1
- Met Lys Gly Asn Met Lys Val Tyr Trp Ile Lys Ile Ala Val Ala Thr
- Trp Phe Cys Cys Thr Thr Ile Val Leu Gly Ser Thr Ala Arg Ile Phe 20 25 30
- Ser Leu Pro Thr Asn Asp Glu Glu Glu Thr Ser Lys Thr Leu Gly Leu 35 40 45
- Asp Thr Val Ser Phe Ser Thr Lys Gly Ala Thr Tyr Ile Thr Tyr Val
- Asn Phe Leu Asn Glu Leu Arg Val Lys Leu Lys Pro Glu Gly Asn Ser
  65 70 75 80
- His Gly Ile Pro Leu Leu Arg Lys Lys Cys Asp Asp Pro Gly Lys Cys
  85 90 95
- Phe Val Leu Val Ala Leu Ser Asn Asp Asn Gly Gln Leu Ala Glu Ile 100 105 110
- Ala Ile Asp Val Thr Ser Val Tyr Val Val Gly Tyr Gln Val Arg Asn 115 120 125
- Arg Ser Tyr Phe Phe Lys Asp Ala Pro Asp Ala Ala Tyr Glu Gly Leu 130 135 140
- Phe Lys Asn Thr Ile Lys Thr Arg Leu His Phe Gly Gly Ser Tyr Pro
- Ser Leu Glu Gly Glu Lys Ala Tyr Arg Glu Thr Thr Asp Leu Gly Ile

Glu Pro Leu Arg Ile Gly Ile Lys Lys Leu Asp Glu Asn Ala Ile Asp 180 185 190

Asn Tyr Lys Pro Thr Glu Ile Ala Ser Ser Leu Leu Val Val Ile Gln 195 200 205

Met Val Ser Glu Ala Ala Arg Phe Thr Phe Ile Glu Asn Gln Ile Arg 210 215 220

Asn Asn Phe Gln Gln Arg Ile Arg Pro Ala Asn Asn Thr Ile Ser Leu 225 230 235 240

Glu Asn Lys Trp Gly Lys Leu Ser Phe Gln Ile Arg Thr Ser Gly Ala 245 250 255

Asn Gly Met Phe Ser Glu Ala Val Glu Leu Glu Arg Ala Asn Gly Lys 260 265 270

Lys Tyr Tyr Val Thr Ala Val Asp Gln Val Lys Pro Lys Ile Ala Leu 275 280 285

Leu Lys Phe Val Asp Lys Asp Pro Lys Thr Ser Leu Ala Ala Glu Leu 290 295 300

Ile Ile Gln Asn Tyr Glu Ser Leu Val Gly Phe Asp 305 310 315

<210> 2 <211> 1176

<212> DNA

<213> Gelonium multiflorum

<400> 2

cagcttctca cttgtttggg ataatgaaag ggaacatgaa ggtgtactgg attaagattg 60 ctgtggcgac atggttttgc tgcactacta ttgtacttgg atcaacggcg aggattttct 120 ctcttcccac aaatgatgaa gaagaaacca gtaagacgct tggcctggac accgtgagct 180 ttagcactaa aggtgccact tatattacct acgtgaattt cttgaatgag ctacgagtta 240 aattgaaacc cgaaggtaac agccatggaa tcccattgct gcgcaaaaaa tgtgatgatc 300 ctggaaagtg tttcgttttg gtagcgcttt caaatgacaa tggacagttg gcggaaatag 360 ctatagatgt tacaagtgtt tatgtggtgg gctatcaagt aagaaacaga tcttacttct 420 ttaaagatgc tccagatgct gcttacgaag gcctcttcaa aaacacaatt aaaacaagac 480 ttcattttgg cggcagctat ccctcgctgg aaggtgagaa ggcatataga gagacaacag 540 acttgggcat tgaaccatta aggattggca tcaagaaact tgatgaaaat gcgatagaca 600 attataaacc aacggagata gctagttctc tattggttgt tattcaaatg gtgtctgaag 660 cagetegatt cacetttatt gagaaccaaa ttagaaataa ettteaacag agaattegee 720 cggcgaataa tacaatcagc cttgagaata aatggggtaa actctcgttc cagatccgga 780 catcaggtgc aaatggaatg ttttcggagg cagttgaatt ggaacgtgca aatggcaaaa 840 aatactatgt caccgcagtt gatcaagtaa aacccaaaat agcactcttg aagttcgtcg 900 ataaagatcc taaaacgagc cttgctgctg aattgataat ccagaactat gagtcattag 960 tgggctttga ttagtacaac ttattgtgct ttttatatat tatagatatg atgccgggcc 1020 atgtattggc cttcgtagct taaataaagg catcgaatat tagcctcggt ggtgtatcta 1080 tcatgctgtg ttgtaaaact gccaatgttt atgttatcaa acagaaattg gcatgaagtt 1140 1176 tctgtacaag tgttcaataa actgggctat acatgc

4948686.1

```
<210> 3
<211> 33
<212> DNA
<213> Homo sapiens
<400> 3
                                                                    33
gctgcccaac cagccatggc ggacattgtg atg
<210> 4
<211> 50
<212> DNA
<213> Homo sapiens
<400> 4
                                                                    50
gccggagcct ggcttgcacg ctgccgctgg tggagccttt gatcatccag
<210> 5
<211> 45
<212> DNA
<213> Homo sapiens
<400> 5
                                                                    45
aagccaggct ccggcgaagg cagcaccaaa ggcgaagtga aggtt
<210> 6
<211> 30
<212> DNA
<213> Homo sapiens
<400> 6
                                                                     30
gccaccgcca ccactagttg aggagactgt
<210> 7
<211> 51
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      Primer
<400> 7
ggcggtggct ccgtcatgac ggacattgtg atgacccagt ctcaaaaaatt c
                                                                     51
<210> 8
<211> 33
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Synthetic
```

## Primer

<400> 8 ggtggcggtg gctccggtct agacaccgtg acg													
<210> 9 <211> 45 <212> DNA <213> Artificial Sequence													
<220> <223> Description of Artificial Sequence: Synthetic Primer													
<400> 9 aaggetegtg tegacetega gteattaage tttaggatet ttate													
<210> 10 <211> 1527 <212> DNA <213> Artificial Sequence													
<220> <223> Description of Artificial Sequence: Synthetic													
<220> <221> CDS <222> (1)(1521)													
<pre>&lt;400&gt; 10 atg acg gac att gtg atg acc cag tct caa aaa ttc atg tcc aca tca Met Thr Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser</pre>	48												
gta gga gac agg gtc agc gtc acc tgc aag gcc agt cag aat gtg gat Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Asp 20 25 30	96												
act aat gta gcc tgg tat caa caa aaa cca ggg caa tct cct gaa cca Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Glu Pro 35 40 45	144												
ctg ctt ttc tcg gca tcc tac cgt tac act gga gtc cct gat cgc ttc Leu Leu Phe Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Asp Arg Phe 50 55 60	192												
aca ggc agt gga tct ggg aca gat ttc act ctc acc atc agc aat gtg Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val 65 70 75 80	240												
cag tot gaa gac ttg goa gag tat tto tgt cag caa tat aac ago tat Gln Ser Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr 85 90 95	288												
cct ctg acg ttc ggt gga ggc acc aag ctg gag atc aaa ggc tcc acc	336												
4948686.1													

Pro	Leu	Thr	Phe 100	Gly	Gly	Gly	Thr	Lys 105	Leu	Glu	Ile	Lys	Gly 110	Ser	Thr	
agc Ser	ggc Gly	agc Ser 115	ggt Gly	aag Lys	cca Pro	ggc Gly	tcc Ser 120	ggc Gly	gaa Glu	ggc Gly	agc Ser	acc Thr 125	aaa Lys	ggc Gly	gaa Glu	384
gtg Val	aag Lys 130	gtt Val	gag Glu	gag Glu	tct Ser	gga Gly 135	gga Gly	ggc Gly	ttg Leu	gtg Val	caa Gln 140	cct Pro	gga Gly	gga Gly	tcc Ser	432
atg Met 145	aaa Lys	ctc Leu	tcc Ser	tgt Cys	gtt Val 150	gtc Val	tct Ser	gga Gly	ttc Phe	act Thr 155	ttc Phe	ggt Gly	aat Asn	tac Tyr	tgg Trp 160	480
atg Met	aac Asn	tgg Trp	gtc Val	cgc Arg 165	cag Gln	tct Ser	cca Pro	gag Glu	aag Lys 170	ggg Gly	ctt Leu	gag Glu	tgg Trp	att Ile 175	gca Ala	528
gaa Glu	att Ile	aga Arg	ttg Leu 180	aaa Lys	tcc Ser	aat Asn	aat Asn	ttt Phe 185	gca Ala	aga Arg	tat Tyr	tat Tyr	gcg Ala 190	gag Glu	tct Ser	576
gtg Val	aaa Lys	999 Gly 195	agg Arg	ttc Phe	acc Thr	atc Ile	tca Ser 200	aga Arg	gat Asp	gat Asp	tcc Ser	aaa Lys 205	agt Ser	agt Ser	gtc Val	624
tac Tyr	ctg Leu 210	caa Gln	atg Met	atc Ile	aac Asn	cta Leu 215	aga Arg	gct Ala	gaa Glu	gat Asp	act Thr 220	ggc Gly	att Ile	tat Tyr	tac Tyr	672
tgt Cys 225	acc Thr	agt Ser	tat Tyr	ggt Gly	aac Asn 230	tac Tyr	gtt Val	Gly aaa	cac His	tat Tyr 235	ttt Phe	gac Asp	cac His	tgg Trp	ggc Gly 240	720
caa Gln	ggc Gly	acc Thr	act Thr	ctc Leu 245	acc Thr	gtc Val	tcc Ser	tca Ser	gct Ala 250	agc Ser	ggt Gly	ggc Gly	ggt Gly	ggc Gly 255	tcc Ser	768
ggt Gly	cta Leu	gac Asp	acc Thr 260	gtg Val	agc Ser	ttt Phe	agc Ser	act Thr 265	aaa Lys	ggt Gly	gcc Ala	act Thr	tat Tyr 270	att Ile	acc Thr	816
tac Tyr	gtg Val	aat Asn 275	Phe	ttg Leu	aat Asn	gag Glu	cta Leu 280	Arg	gtt Val	aaa Lys	ttg Leu	aaa Lys 285	ccc Pro	gaa Glu	ggt Gly	864
aac Asn	agc Ser 290	His	gga Gly	atc Ile	cca Pro	ttg Leu 295	Leu	cgc Arg	aaa Lys	aaa Lys	tgt Cys 300	Asp	gat Asp	cct	gga Gly	912
aag Lys 305	Cys	ttc Phe	gtt Val	ttg Leu	gta Val 310	Ala	ctt Leu	tca Ser	aat Asn	gac Asp 315	Asn	gga Gly	cag Gln	ttg Lev	gcg Ala 320	960
gaa Glu	ı ata ı Ile	gct Ala	ata Ile	gat Asp	gtt Val	aca Thr	agt Ser	gtt Val	tat Tyr	gt <u>c</u> Val	g gtg Val	ggc Gly	tat Tyr	caa Glr	ı gta ı Val	1008

325 330 335

aga Arg	aac Asn	aga Arg	tct Ser 340	tac Tyr	ttc Phe	ttt Phe	aaa Lys	gat Asp 345	gct Ala	cca Pro	gat Asp	gct Ala	gct Ala 350	tac Tyr	gaa Glu	1056
ggc Gly	ctc Leu	ttc Phe 355	aaa Lys	aac Asn	aca Thr	att Ile	aaa Lys 360	aca Thr	aga Arg	ctt Leu	cat His	ttt Phe 365	ggc Gly	ggc Gly	agc Ser	1104
tat Tyr	ccc Pro 370	tcg Ser	ctg Leu	gaa Glu	ggt Gly	gag Glu 375	aag Lys	gca Ala	tat Tyr	aga Arg	gag Glu 380	aca Thr	aca Thr	gac Asp	ttg Leu	1152
ggc Gly 385	att Ile	gaa Glu	cca Pro	tta Leu	agg Arg 390	att Ile	ggc Gly	atc Ile	aag Lys	aaa Lys 395	ctt Leu	gat Asp	gaa Glu	aat Asn	gcg Ala 400	1200
ata Ile	gac Asp	aat Asn	tat Tyr	aaa Lys 405	cca Pro	acg Thr	gag Glu	ata Ile	gct Ala 410	agt Ser	tct Ser	cta Leu	ttg Leu	gtt Val 415	gtt Val	1248
att Ile	caa Gln	atg Met	gtg Val 420	tct Ser	gaa Glu	gca Ala	gct Ala	cga Arg 425	ttc Phe	acc Thr	ttt Phe	att Ile	gag Glu 430	aac Asn	caa Gln	1296
att Ile	aga Arg	aat Asn 435	aac Asn	ttt Phe	caa Gln	cag Gln	aga Arg 440	att Ile	cgc Arg	ccg Pro	gcg Ala	aat Asn 445	aat Asn	aca Thr	atc Ile	1344
agc Ser	ctt Leu 450	gag Glu	aat Asn	aaa Lys	tgg Trp	ggt Gly 455	aaa Lys	ctc Leu	tcg Ser	ttc Phe	cag Gln 460	atc Ile	cgg Arg	aca Thr	tca Ser	1392
ggt Gly 465	gca Ala	aat Asn	gga Gly	atg Met	ttt Phe 470	tcg Ser	gag Glu	gca Ala	gtt Val	gaa Glu 475	ttg Leu	gaa Glu	cgt Arg	gca Ala	aat Asn 480	1440
ggc	aaa Lys	aaa Lys	tac Tyr	tat Tyr 485	gtc Val	acc Thr	gca Ala	gtt Val	gat Asp 490	Gln	gta Val	aaa Lys	ccc Pro	aaa Lys 495	ata Ile	1488
gca Ala	ctc Leu	ttg Leu	aag Lys 500	Phe	gtc Val	gat Asp	aaa Lys	gat Asp 505	cct Pro	aaa Lys	. taa	tga.				1527

<210> 11

<211> 507

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic

<400> 11

Met Thr Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser 1 5 10 15

Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Asp 20 25 30

Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Glu Pro 35 40 45

Leu Leu Phe Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Asp Arg Phe 50 55 60

Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val 65 70 75 80

Gln Ser Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr 85 90 95

Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr

Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu
115 120 125

Val Lys Val Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser 130 135 140

Met Lys Leu Ser Cys Val Val Ser Gly Phe Thr Phe Gly Asn Tyr Trp 145 150 155 160

Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Ala 165 170 175

Glu Ile Arg Leu Lys Ser Asn Asn Phe Ala Arg Tyr Tyr Ala Glu Ser 180 185 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ser Val 195 200 205

Tyr Leu Gln Met Ile Asn Leu Arg Ala Glu Asp Thr Gly Ile Tyr Tyr 210 215 220

Cys Thr Ser Tyr Gly Asn Tyr Val Gly His Tyr Phe Asp His Trp Gly 225 230 235 240

Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Gly Gly Gly Ser 245 250 255

Gly Leu Asp Thr Val Ser Phe Ser Thr Lys Gly Ala Thr Tyr Ile Thr 260 265 270

Tyr Val Asn Phe Leu Asn Glu Leu Arg Val Lys Leu Lys Pro Glu Gly 275 280 285

Asn Ser His Gly Ile Pro Leu Leu Arg Lys Lys Cys Asp Asp Pro Gly

Lys Cys Phe Val Leu Val Ala Leu Ser Asn Asp Asn Gly Gln Leu Ala 305 310 315 320

- Glu Ile Ala Ile Asp Val Thr Ser Val Tyr Val Val Gly Tyr Gln Val 325 330 335
- Arg Asn Arg Ser Tyr Phe Phe Lys Asp Ala Pro Asp Ala Ala Tyr Glu 340 345 350
- Gly Leu Phe Lys Asn Thr Ile Lys Thr Arg Leu His Phe Gly Gly Ser
- Tyr Pro Ser Leu Glu Gly Glu Lys Ala Tyr Arg Glu Thr Thr Asp Leu 370 375 380
- Gly Ile Glu Pro Leu Arg Ile Gly Ile Lys Lys Leu Asp Glu Asn Ala 385 390 395
- Ile Asp Asn Tyr Lys Pro Thr Glu Ile Ala Ser Ser Leu Leu Val Val 405 410 410
- Ile Gln Met Val Ser Glu Ala Ala Arg Phe Thr Phe Ile Glu Asn Gln 420 425 430
- Ile Arg Asn Asn Phe Gln Gln Arg Ile Arg Pro Ala Asn Asn Thr Ile
  435
  440
  445
- Ser Leu Glu Asn Lys Trp Gly Lys Leu Ser Phe Gln Ile Arg Thr Ser 450 455 460
- Gly Ala Asn Gly Met Phe Ser Glu Ala Val Glu Leu Glu Arg Ala Asn 465 470 475 480
- Gly Lys Lys Tyr Tyr Val Thr Ala Val Asp Gln Val Lys Pro Lys Ile 485 490 495
- Ala Leu Leu Lys Phe Val Asp Lys Asp Pro Lys 500 505